STATUS OF THE CLAIMS

Claim 1 has been amended herein to correct a typographic error. Claim 10 has been amended in view of the election below. Claim 11 is cancelled in view of the amendment to claim 10. Claims 15, 18, 22-27, and 31-36 are canceled as drawn to non-elected subject matter. Applicants note that although claim 36 is included in Group I, the recited polynucleotide sequences do not encode a TTG1, and hence the claim has been cancelled in view of the election below. Applicants reserve the right to prosecute non-elected subject matter in one or more continuing application(s).

RESPONSE TO RESTRICTION REQUIREMENT

In response to the restriction requirement which the Examiner imposed, Applicants elect, with traverse, to prosecute claims 1-13, 19-21, 28-30 and 36, *i.e.*, the Group I claims. With respect to the requirement to elect a single nucleic acid for examination, Applicants elect nucleic acids encoding TTG1, and further elect, with traverse, SEQ ID NO:147.

Traversal is made on the basis that the Group II claims (claims 14 and 16-17) should be examined together with the Group I claims. Specifically, these claims are directed to a food product, meal or feed produced from the seed of claim 13, respectively. Claim 13 is included in the Group I claims and includes as a point of novelty a TTG1 nucleotide as introduced according the elected method of claim 10. A food product, meal or feed produced from this seed according to the elected invention would therefore include the genetic material of the seed and thus also contain the TTG1 nucleotide.

Therefore, once the TGG1 nucleic acid in claim 10 is found to be novel and nonobvious, each of claims 14 and 16-17 inherently including this element would by definition necessarily be novel and nonobvious without the need for *any* search. Specifically, the nucleic acid forms an

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inherent element of these claims, the absence of which from the prior art renders the claims novel and nonobvious.

The M.P.E.P. requires that "[i]f the search and examination of an entire application can be made without serious burden, the examiner *must* examine it on the merits, even though it includes claims to independent or distinct inventions." (emphasis added) M.P.E.P. §803. Here, an examination of the Group II claims together with the Group I claims would cause no additional burden because these claims incorporate the limitations of the Group I claims. Examination of the Group I and II claims is thus respectfully requested.

Traversal is also made regarding election of the single sequence SEQ ID NO:147 on the basis that, despite the Examiner's assertion that the described TTG1 genes (SEQ ID NOs:2, 3, and 147) are "not a member of a single structurally and functionally related genus", the specification clearly describes them as such. For instance, at page 44, Example 7, the soybean and corn sequences were identified based on their similarity with a TTG1 encoding sequence. A comparison of SEQ ID NO:2 and SEQ ID NO:147 (attached as exhibit A) confirms that they share 77-80% sequence similarity over a substantial portion of the two sequences covering more than 90% of SEQ ID NO:147. Comparison of SEQ ID NO:3 and SEQ ID NO:147 also indicates greater than 75% sequence similarity over substantial portions of the sequences. Examination of the nucleic acids comprising a TTG1-encoding nucleotide is thus respectfully requested.

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The Examiner is invited to contact the undersigned attorney at (512) 536-3085 with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,

Ron J. Lely, Reg# 53,173, for

Robert E. Hanson
Reg. No. 42,628
Attorney for Applicants

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600 Congress Avenue, Suite 2400
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(512) 474-5201

Date: August 30, 2006

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PAGE 8/13 * RCVD AT 8/30/2006 7:51:52 PM [Eastern Daylight Time] * SVR:USPTO-EFXRF-6/28 * DNIS:2738300 * CSID:512 536 4598 * DURATION (mm-ss):02-14

EXHIBIT A

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   View option Standard

Masking character option X for protein, n for nucleotide ▼   Masking color option Black

☐ Show CDS translation

Sequence 1: lcl|2
Length = 1405 (1 .. 1405)

Sequence 2: lcl|147
Length = 1035 (1 .. 1035)
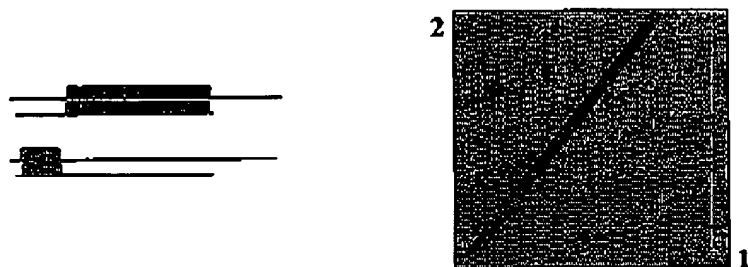
NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.


```
 Score =  456 bits (237),  Expect = 1e-124
 Identities = 566/728 (77%), Gaps = 6/728 (0%)
 Strand=Plus/Plus

Query  315  GACCTCCTCGCCACCTCCGGCGACTACCTCCGCCTCTGGGAGATCCGTGATAACTCC----  371
            |||||||||||||| ||||||||||||| |||||||||||||||| ||    || |||||
Sbjct  286  GACCTCCTCGCCTCCTCCGGCGACTTCCTCCGCCTCTGGGAGGTCAACGAAGACTCCTCC  345

Query  372  ---GTGGATGCCGTCTCCCTCTTCAACAACAGCAAGACCAGCGAGTTCTGCGCCCCCTTA  428
               | ||| | || || || ||||||||||||||| |||||||||||||| || |
Sbjct  346  TCCGCGGAGCCAGTATCGGTCCTCAACAACAGCAAGACGAGCGAGTTCTGCGCGCCGCTG  405

Query  429  ACCTCTTTCGACTGGAACGACATCGACCCCAACCGCATCGCCACCTCCAGCATCGACACC  488
            ||||| |||||||||||||||||||| | || || || || | | ||| | |||||||||||||||
```

```
Sbjct  406   ACCTCCTTCGACTGGAACGACGTGGAGCCGAAGCGGTTAGGCACGTGCAGCATCGACACC   465

Query  489   ACCTGCACCATCTGGGACATCGAACGCACCCTCGTCGAAACCCAACTCATCGCTCACGAC   548
             || |||||| ||||||||| | || | || | || || !| || || |||||||| |||||||
Sbjct  466   ACGTGCACGATCTGGGACGTGGAGAGGTCCGTGGTGGAGACGCAGCTCATCGCGCACGAC   525

Query  549   AAGGAGGTTTACGACATCGCCTGGGGAGAGGCCAGAGTCTTCGCCTCCGTCTCCGCCGAC   608
             ||||||||  |||||||||| ||||| ||||| || || |||||||| ||||||||||||
Sbjct  526   AAGGAGGTCCACGACATCGCGTGGGGGGGAGGCTAGGGTTTTCGCCTCGGTCTCCGCCGAC   585

Query  609   GGCTCCGTTAGAATCTTCGACCTTCGCGACAAGGAGCACTCCACCATCATCTACGAGAGC   668
             || || || || || |||||||| || |||||||||||||||||||||||||||||||||||
Sbjct  586   GGATCGGTGAGGATCTTCGATCTGCGCGACAAGGAGCACTCCACCATCATCTACGAGAGC   645

Query  669   CCCCACCCTGACACCCCTTTGCTCCGCTTGGCTTGGAACAAACAGGACCTGAGGTACATG   728
             ||||| || || || || || | || ! | || ||||||||| |||||| || ||| |||
Sbjct  646   CCCCAGCCCGATACGCCGCTCCTGAGGCTCGCGTGGAACAAGCAGGACTTGCGGTGTATG   705

Query  729   GCCACCATTTTAATGGACAGTAATAAAGTTGTGATTTTGGATATTAGGTCTCCCACTACC   788
             |||||.|||| | ||||| |||! |||!| ||| | || ||| ! || || || ! ! |
Sbjct  706   GCCACGATTCTGATGGATTCGAATAAGGTTGTCATTCTCGACATTCGATCGCCGACGATG   765

Query  789   CCTGTTGCGGAGTTAGAGAGGCACCGTGGGAGTGTGAACGCCATTGCTTGGGCTCCTCAT   848
             || || || ||| | | || ||||||| ||||!||||||||||| |!||! !|||| || ||
Sbjct  766   CCGGTCGCCGAGCTTGAAAGGCACCAGGGGAGTGTGAACGCGATTGCGTGGGCGCCGCAG   825

Query  849   AGCTCCACGCATATTTGTTCTGCTGGTGATGATACTCAGGCTCTTATTTGGGAATTGCCC   908
             |||| | ||||||| || || | ||| ||||| | |||||||||| ||||| |||||
Sbjct  826   AGCTGTAAGCATATCTGCTCGGGTGGGGATGACGCGCAGGCTCTTATCTGGGAGTTGCCG   885

Query  909   ACGCTTGCTTCTCCCACTGGGATTGATCCCGTCTGCATGTACTCTGCTGGCTGTGAAATT   968
             ||| | |||   || | ||||||||||||||| | |  | ||||| || || | || |||
Sbjct  886   ACGATGGCTGGGCCGAATGGGATTGATCCCATGTCGGTTTACTCGGCCGGTTCGGAGATT   945

Query  969   AACCAGCTGCAGTGGTCCGCCGCCCAGCCCGATTGGATTGCCATTGCTTTTGCCAACAAG   1028
             ||||||  ||||||||||| || | | ||| ||||||||||| |||!|| ||||| |||||
Sbjct  946   AACCAGTTGCAGTGGTCGGCTTCTCTGCCTGATTGGATTGGCATTGCGTTTGCTAACAAA   1005

Query  1029  ATGCAGCT   1036
             ||||||||
Sbjct  1006  ATGCAGCT   1013
```

Score = 156 bits (81), Expect = 2e-34
Identities = 170/212 (80%), Gaps = 3/212 (1%)
Strand=Plus/Plus

```
Query  70    GATCGGAAAACTCCGTCACTTACGAGTCCCCTTACCCTATCTACGGCATGTCATTCTCCC   129
             |||||||||| | |||||||| ||||| || || !!||| |||||| ||||| |||||||
Sbjct  44    GATCGGAAACCGCCGTCACCTACGACTCTCCGTACCCGCTCTACGCCATGTCCTTCTCCT   103

Query  130   CCTCCCACCCCCACCGCCTCGCCCTCGGCAGCTTCATCGAAGAATACAACAACCGCGTCG   189
             |||||     ||||||| |||||  |||| |||||||| |||| || ||||||||||| |||
Sbjct  104   CCTCCA---CCCACCGAATCGCCGTCGGGAGCTTCCTCGAGGACTACAACAACCGCATCG   160
```

```
Query  190  ACATCCTCTCTTTCCACCCTGACACCCTTTCGGTAACTCCCCACCCTTCTCTCTCCTTCG  249
            |||||||||| ||| || | ||| || | ||  | |  |||| || || |||||||||||
Sbjct  161  ACATCCTCTCCTTCGACTCCGACTCCATGTCCCTCAAGCCCCTTCCATCCCTCTCCTTCG  220

Query  250  ACCACCCTTACCCTCCCACCAAACTCATGTTC  281
            | ||||||||||||||||||||| ||||||||
Sbjct  221  AGCACCCTTACCCTCCCACCAAGCTCATGTTC  252
```

CPU time: 0.02 user secs.   0.00 sys. secs   0.02 total secs.

```
Lambda      K       H
   1.33     0.621    1.12

Gapped
Lambda      K       H
   1.33     0.621    1.12
```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 61
Number of extensions: 6
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Length of query: 1405
Length of database: 17,788,496,656
Length adjustment: 27
Effective length of query: 1378
Effective length of database: 17,788,496,629
Effective search space: 24512548354762
Effective search space used: 24512548354762
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)